Kemmerer, Elizabeth

From:

Kemmerer, Elizabeth

Sent:

Thursday, June 19, 2003 2:29 PM

To: Subject: Kunz, Gary SPDI favor

Importance:

High

Hi Gary-

I am currently working on 09/941992, a SPDI case which is a date case. The 2 companion cases are not yet docketed: 09/990711 and 09/991150. They're both in central files on the 12th floor. Can these be docketed to me as well, since it would be easy to write up the 3 cases together, and they're all date cases?

Thanks a bunch,

Elizabeth (Betsy) Kemmerer Art Unit 1646 308-2673 CM1-10B17 Mailbox: 10D19

STIC-Biotech/ChemLib

From: Sent:

Kemmerer, Elizabeth Thursday, June 19, 2003 2:30 PM STIC-Biotech/ChemLib

To: Subject:

sequence search request

Please search SEQ ID NO: 20 for 09/941992; regular and interference, please.

Thanks,

Elizabeth (Betsy) Kemmerer Art Unit 1646 308-2673 CM1-10B17 Mailbox: 10D19

Mary Jane Ruhl
Tech. Info. Specialist, STIC TC-1600 CM-1, Room 6A-06

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This represents a human secreted protein. The specification provides secreted protein sequences (AAM63681 to AAW6369) encoded by the nucleic acid sequences shown in AAV43601 to AAV43699. The invention provides a method of identifying a secreted polypeptide which is modified by rough microsomes. The secreted proteins can be used in assays to determine biological activities, such as cytokine, cell proliferation, or cellular differentiation activity, resemptor/ligand activity, haemostatic or chmombolytic activity, receptor/ligand activity, haemostatic or thrombolytic activity, receptor/ligand activity, tumour inhibition, or anti-inflammatory activity. The proteins can also be used as biomarkers, to identify tissues or cell types which express the proteins, or a stage- or disease-specific alteration in protein expression. They proteins. Compounds which affect the biological activities of the secreted proteins or their ability to interact with specific ligands can be identified using the proteins in screening assays. The proteins and antibodies that bind specifically, to the protein can also be used to be identified using therefore the protein can also be used to be identified dispositions for diseases which are the compounds which hereapeutic compositions for diseases which
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Matches 362; Conservative
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AAY73325-Y73389 are human transcriptional regulator molecule (HTRM)

protein sequences. The HTRM protein and nucleotide sequences are useful

Cor preventing or treating disorders associated with decreased expression

or activity of HTRW which include cell proliferative disorders such as

carteriosclerosis and cirrhosis; cancers including adenocarcinoma and

arteriosclerosis and cirrhosis; cancers including adenocarcinoma and

carteriosclerosis, and myasthenis; multiple sclerosis, systemic lupus

mellitus, rheumatoid arthritis, multiple sclerosis, systemic lupus

crythematosus, and myasthenia gravis; infections and trauma. Antagonists

of the HTRM polypeptides are useful for treating or preventing disorders

associated with increased expression or activity of HTRMs. HTRM

colypeptides, their immunogenic fragments or oligopeptides are useful

cor screening libraries of compounds in drug screening techniques.

Polynucleotides encoding HTRM are useful for blocking the transcription

of mRNA and regulating gene function by modulating the transcription

of mRNA and regulating gene function by modulating the transcription

of mRNA and regulating gene function by modulating the transcription

of mRNA and regulating gene function by modulating the transcription

of mRNA and regulating gene function by modulating the transcription

of mRNA and regulating dene function by modulating the transcription

of mRNA and regulating dene function by modulating the transcription

of mRNA and regulating dene function by modulating the transcription

of mRNA and regulating dene function by modulating the transcription

of mRNA and regulating defected with the expression of HTRM, uncleotides

cracking and ansociated with the expression of HTRM manner was the manner was the procession of HTRM manner was the procession of the proc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences encoding HTRM may be useful to generate hybridization probes useful in mapping the naturally occurring genomic sequence and to detect differences in gene sequences among normal, carrier and affected individuals. Using diagnostic assays, cancer can be detected prior the appearance of clinical symptoms and thereby progression of cancer can be prevented by aggressive treatment or preventive measures.
                                                                                                                                                                                                                                                                                                                                                                                HTRM; human transcriptional regulatory molecule; arteriosclerosis; AIDS; arteriosolesosis; cirrhosis; cancer; leukaemia; diabetes mellitus; Addison's disease; multiple sclerosis; rhematoid arthritis; infection; trauma; myasthenia gravis; adenocarcinoma; immune disorder; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptides useful for diagnosis, prevention and treatment of cancer immune disorders
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Lu DAM;
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Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H,
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Patterson C, Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 129-130; 193pp; English
435 QALRDEASSSGCSETDSTELASIL 458
                          151 QALRDEASSGCSETDSTELASIL 374
                                                                                                                                                                                                                                                                                                                              HTRM clone 156986 protein sequence.
                                                                                                                                                                            AAY73370 standard; Protein; 530 AA
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98US-0102745.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-052941/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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02-OCT-1998;
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Gerstin EH,
                                                                                                                                                                                                                              AAY73370;
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530 AA;

Sequence

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26-JUN-2001 (first entry)
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                                                                                                                                                                                        The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are calcal conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune through arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILILGVRE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLGFR 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEFONLLLAIMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLIITYA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 TLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRRQNKKAL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                               Claim 11; SEQ ID NO 2710; 2081pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1816; DB 23;
Pred. No. 3.8e-163;
5; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362; Conservative
               Rosen CA;
                                           WPI; 2002-122018/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   530 AA;
                                                           N-PSDB; ABL90743
               Birse CE,
                                                                                                                                    disorders
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AAB94114 standard; Protein; 365 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotide which comprises a 3'-end sequence, where the compines at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sare useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs are present man cDNA sequences; AAH03166 to AAH13628 and AAH13639 to AAH13639 represent human amino acid sequences; and AAH13632 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 TCFHV----PYSALTMF-----ISTEQTERDSATAYRMTVEVLGTVLGTAIQGQIVG
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                                                         detection; diagnosis; antisense therapy; gene therapy.
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Otsuki T;
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Pred. No. 3.8e-85;
; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID 14354; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagai K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashi K,
A, Nagai K
Human protein sequence SEQ ID NO:14354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wakamatsu
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27-JMG-1999; 99JP-0300253.
11-JMG-1099; 09JP-0118776.
12-JMAY-2000; 2000JP-01187767.
                                                                                                                                                                                                                                                                                                     28-JUL-2000; 2000EP-0116126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              full-length cDNAs
                                                            primer;
                                                                                                                         Homo sapiens
                                                                                                                                                                               EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUN-2000;
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The polynucleotide sequences given in AAF33213 to AAF33261 encode the human secreted proteins given in AAB64882 to AAB64930. AAB64931 to AAB6491 represent human secreted polypeptide sequences and proteins homeologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: and cells the genes are expressed in. Examples of activities include: and tinflammatory; antisclerotic; dermatological; immunosuppressive; antimicroblal; anti-anglogenic; ophthalmological; cardiant; vascular; antimicroblal; anti-anglogenic; ophthalmological; neuroprotectant; anticonvulsant; nootropic; antialzheimers; antiparkinsonian; and vulnerary. The polynucleotides and polypeptide expression. Disorders that may be be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. Disorders that may be prevented, diagnosed and/or treated by the above methods include immune disorders (e.g. multiple solerosis, systemic lupus erythematosus and human immuno-deficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases (e.g. scimitar syndrome, Chapta's cardiomyopathy and coronary cardiovascular diseases).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), infectious diseases and/or for promoting wound healing, regeneration and /or chemotaxis. AAF33204 to AAF33212 and AAB64881 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            400 MLVTMAPIVLILLGLLLFKMYPIDEERRRQNKKALQALRDEASSSGCSETDSTELASIL 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurological disorder; regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arteriosclerosis), angiogenic disorders (e.g. corneal graft'
neovascularisation and diabetic retinopathy), neurological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding 49 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein sequence encoded by gene 9 SEQ ID NO:125.
                      Huntington's chorea, Alzheimer's disease, Parkinson's disease, infectious disease, chemotaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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100.0%; Pred. No. 2.5e-19;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                 Rosen CA, Ruben SM, Komatsoulis GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB64947 standard; Protein; 173 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 488; 554pp; English.
  corneal graft neovascularisation;
                                                                                                                                                                                                                                                                                                   HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                         11-JUN-1999; · 99US-0138572
                                                                                                                                                                                                                 01-JUN-2000; 2000WO-US14933
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Best Local Similarity 100.
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-071147/08
                                                                                                                                                                                                                                                                                                                         ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAF33221
                                                                                                                          WO200076530-A1.
                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2001
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BX BX BX B
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The polynuclectide sequences given in AAF33213 to AAF33261 encode the human secreted proteins given in AAB64882 to AAB64931 to AAB64931 represent human secreted polypeptide sequences and proteins condeciles the genes are given in the exemplification of the proteins invention. Human secreted proteins have activities based on the tissues can decilis the genes are expressed in the exemplification of the present invention. Human secreted proteins have activities based on the tissues can decilis the genes are expressed in the proteins anti-HIV; immunostimulant; cytostatic; cardiant; antinflammatory; anti-HIV; immunostimulant; cytostatic; cardiant; continflammatory; anti-HIV; immunostimulant; cytostatic; cardiant; continflammatory; anti-HIV; immunostimulant; cytostatic; cardiant; contingues antiparkinsonian; and vulnerary. The polynucleotides and polypeptides can entroprotectant; anticonvulsant; nootropic; antialzheimers; antiparkinsonian; and vulnerary. The polynucleotides and polypeptide can be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. Disorders that may be prevented, diagnosed and/or treated by the above methods include immune calsorders (e.g. multiple sclerosis, systemic lupus expthematosus and channer in mumon deficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiowascular diseases (e.g. cancers and Gaucher's disease and Parkinson's disease), infectious diseases and/or for promoting wound healing, regeneration and concers and concers and dabetic retinopathy, neurological disorders (e.g. unfectious diseases and/or for promoting wound healing, regeneration and chances and/or for promoting wound healing, regeneration and chances and/or for promoting wound healing, regeneration and concers and concers and/or for promoting wound healing, regeneration and concers and concers and parkinson's diseases and or chemotaxis. AAF33204 to AAF33212 and AAB64881 represent sequences and parking concerned a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dermatological; immunosuppressive; antiinflammatory; anti-HIV; immunostimulant; cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological; neuroprotectant; nootropic; anticonvulsant; vulnerary;
                                                                                                                                                                                                                                  coronary arteriosclerosis; angiogenic disorder; diabetic retinopathy; corneal graft neovascularisation; neurological disorder; regeneration; Huntington's chorea; Alzheimer's disease; Parkinson's disease;
                                                                                                                     antialzheimers; antiperkinsonian; antimicrobial; immune disorder;
antialzheimers; antiperkinsonian; antimicrobial; immune disorder;
multiple sclerosis; systemic lupus erythematosus; HIV; infection;
hyperproliferative disorder; cancer; Gaucher's disease; wound healing;
cardiovascular disease; Scimitar syndrome; Chaga's cardiomyopathy;
                         Human; secreted protein; diagnosis; immunomodulatory; antisclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding 49 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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66.2%; Pred. No. 2.7e-10;
tive 5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 525; 554pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Komatsoulis
                                                                                                                                                                                                                                                                                                                   infectious disease; chemotaxis.
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(ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0138572.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA, Ruben SM,
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                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Olsen HS,
   Lafleur DW,
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AAE10448
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                                                   13;
                                                                                                                                                                  253 FRNEFQNLLLAIMLSATL-TIPIWQWFLTRFGKKTAVYVG-ISSAVPFLILVALMESNLI 310
                                                                                                                                                                                                         DIGLETVLVLVQNLVGTVASAPLVPGMYARIGKKNTFLIGALLGTCGYLLFFWSVWSLP 320
                                                                     73 IGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVLGTAIQGQI 132
                                                                                                                                                                                                                                                                                       LGLCYSLVNIPYGSLATAMT00--POSRARLGAARGIAAS--LTFVCLAFLIGPSIK--- 171
                                                                                                                                 204
                                                                                                                                                    193 REQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLG 252
                                                                                                                                                                                                                                   311 ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHG-----TEPIFFSFYVFFT 363
                                                                                                                                                                                                                                                                           KFASGVSLGISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPID 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AlDS; leukaemia;
                                                                                                                                                                                                                                                       VALVALAIASIGOGVTMTVMWALEADTVE-----YGEYLTGVRIEGLTYSLFSFTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ebner R;
                                                                                                            133 VGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILILGV
                                                                                                                               -----NSSPEEMVSVYH------FWTIVLAIAGMV--LYFIC----FKST
                                                   Gaps
                                                   63;
                               Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Florence KA;
Mucenski M,
                             Score 143.5; DB 19; Length; Pred. No. 7.5e-05; 62; Mismatches 178; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Young PE,
Carter KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein HKFBC53, SEQ ID NO:145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ni J, Rosen CA, Wei Y,
Brewer LA, Endress GA,
                                                                                                                                                                                                                                                                                                                                                                                       AAY86230 standard; Protein; 443 AA.
                                                                                                                                                                                                                                                                                                                                     DKKFKEIVVEIDNRKKVQ 448
                                                                                                                                                                                                                                                                                                                   EERRRO-----435
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98US-0089508.
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98US-0090112.
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                             6.0%;
19.8%;
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                                                  Conservative
                                       Similarity
         457 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ni J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09966041-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Soppet DR,
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          Sequence
                            Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357
                                                                                                                                                                                                                                                                                                               AAZ97019 to AAZ97137 represent 94 isolated human secreted protein genes. AAX86215 to AAY86333 are the secreted proteins encoded by the 94 human genes. This sequence represents a fragment of one of the human secreted proteins. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 94 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developmental abnormalities and foctal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney disorders, dispestive-bendocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. The sequences shown in AAY86334 to AAY86585 represent fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 -DVPVFRNLS-----GAVFSLLFHLGTRER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 AQGLAPGRHRLRPAVLPLHLQPLPGLWGGHAEWAALLYYGPFIVIFQFGWASTQISHLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 ADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILLLGVREQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 138; Gaps
                                                                                                  New isolated human genes and the secreted polypeptides they encoduseful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 132; DB 21;
; Pred. No. 0.00089;
46; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 SSGSCPTSHTARPIGTCFSIASL-----KQWSRVSMF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---PHTNSGXFVYGSM-SFLDKVANGLAV 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343 LKQPHFHGTEPIFFSFYVFFTKFASGVSL 371
                                                                                                                                                                                                                                                  Claim 1; Page 400-402; 586pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE10448 standard; Protein; 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.5%
Best Local Similarity 19.8%
Matches 77; Conservative
WPI; 2000-106100/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secreted proteins.
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                              N-PSDB; AAZ97034
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June 19, 2003, 17:46:17; Search time 26 Seconds (without alignments) 518.296 Million cell updates/sec
                                                                                                                                                                                            US-09-941-992-20
2384
1 WMLRWALSLPPSSCLWAEPG.......DEASSSGCSETDSTELASIL 458
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                              Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                               Scoring table:
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                                                                                                                Run on:
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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Issued_Patents_AA:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

																	-											-
	Description	Sequence 6, Appli	Sequence 6, Appli	Patent No. 5432081		7	7	7	7	7	22	Sequence 19, Appl	Patent No. 5206352	Sequence 12, Appl	Patent No. 5268463	Sequence 5, Appli	Sequence 5, Appli		Sequence 2, Appli	Sequence 2, Appli	Sequence 3507, Ap	Patent No. 5268463	Patent No. 5432081	Sequence 4893, Ap	Sequence 6, Appli	Sequence 15, Appl		
	ID	US-08-882-704A-6	US-09-151-957-6	5432081-7	5432081-9	US-09-416-213-2	US-09-416-214-2	US-09-035-676-2	US-08-752-447-2	US-09-316-167-2	5268463-8	US-08-583-276-19	5206352-4	US-08-677-049-12	5268463-7	US-08-689-974-5	US-09-058-376-5	US-08-684-932A-38	PCT-US96-10618-2	US-08-784-649A-2	US-09-134-001C-3507	5268463-9	5432081-10	US-09-134-001C-4893	US-09-172-353-6	US-09-200-673-15	US-09-134-001C-3105	US-09-045-186-2
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ф	Query	6.0	9.0	5.4	5.1	4.6	4.6	4.6	4.5	4.5	4.5	4.5	4.5	4.4	4.3	4.2	4.2	4.1	4.0	4.0	4.0	4.0	4.0	4.0	3.9	3.9	3.9	3.9
	Score	143.5	143.5	128.5	120.5	109	109	109	107.5	107.5	107	106.5	106.5	106	103	101	101	97.5	96.5	96	95.5	95	95	94.5	93.5	93.5	93	92.5
	Result No.	н	7	3	4	5	9	7	8	Ø	10	11	12	13	14	15	16	17	18	19	20	. 21	22	23	24	25	56	27

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1192.5 92.5 92.5 92.5 92.5 92.5 92.5 92.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5	. 6	ALIGNMENTS d A. J. IDE REPRESSORS AND US LLP er, 701 Fifth Avenue 8-DOS #1.0, Version #1.30 882,704A h.D., Carol 7 90106.404	Score 143.5; DB 2; L Pred. No. 2.1e-05; 62; Mismatches 178; I FPTRLSPCSSATEQTERDSATAYR	: : MTQQPQSRARLGAARGIAAS	SQSANHTHGTTSHRETQKAYLLAA
1192.5 92.5 92.5 92.5 92.5 92.5 92.5 92.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5 91.5	.9 384 1 2 384 2 2 384 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	ion in	6.0%; nilarity 19.8%; Conservative TCFSIASLKQWSRVSM	: : :: : CYSLVNIPYGSLATA	GADTPCFQDFNSSTVA
RESGI GIN OS-O	28 92.5 30 92.5 31 92.5 32 92.5 33 92.5 34 91 35 91 36 91 36 91 37 91 40 89.5 41 89.5 42 88.5 44 88.5 44 88.5	Pat Get OB Dat Get OB	Ouery Match Best Local Si Matches 75;	119	133

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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-416-213-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                      HILLSBOROUGH
                                                        CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94010
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                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -09-416-214-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 IGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRWTVEVLGTVLGTAIQGQI 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 LGLCYSLVNIPYGSLATAMTQQ--PQSRARLGAARGIAAS--LIFVCLAFLIGPSIK--- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 FRNEFQNLLLAIMLSATLTIPIW------QWFLTRFGKKTAVYVG-ISSAVPFLILVA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 LMESNLIITYAVAVAAGISVAAAFILPWSMLPDVIDDFHLKQPHFHG------TEPIFF 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFYVFFTKFASGVSLGISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLL 416
SFYVFFTKFASGVSLGISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLL 416
                                    364 SLFSFTRKCGQAIGGSIPAFILGLSGYIANQVQTPE-VIMGIRTSIALVPCGFMLLAFVI 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 DIGLETVLVL-----VQNPGWYCGIGTAGAXMVARIGKKNTFLIGALLGTCGYLLFFW 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356 SLFSFTRKCGQAIGGSIPAFILGLSGYIANQVQTPE-VINGIRTSIALVPCGFMLLAFVI 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 VGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILLLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 VSVWSLPVALVALAIASIGOGVTMTVMWALEADTVE-----YGEYLTGVRIEGLTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 428;
                                                                                                                                                                                                                                APPLICANT: JEFFERSON, RICHARD A. TITLE OF INVENTION: HOST CELLS TRANSFORMED WITH THE E.COLISCUCORONIDE PERMEASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 120.5; DB 6; Length
; Pred. No. 0.003;
58; Mismatches 173; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suppressors of Death Domains
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,546
FILING DATE: 15-0CT-1993
PRIOR APPLICATION NUMBER: 447,976
FILING DATE: 31-0CT-1989
APPLICATION NUMBER: 264,586
FILING DATE: 31-0CT-1988
APPLICATION NUMBER: 119,102
FILING DATE: 10-NOV-1987
                                                                          417 FKMYPIDEERRRQ-----NKKALQ 435
                                                                                               423 IWFYPLTDKKFKEIVVEIDNRKKVQ 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09416213
Patent No. 6110690
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Goeddel, David V. APPLICANT: Jang, Yingping TITLE OF INVENTION: Suppress NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.1%;
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Best Local Similarity
Matches 71; Conserva
                                                                                                                                                                                                                5432081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 428
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357
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                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                            5432081-9
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HTARPIGTCFSIASLKQWSRVSMFPTRLS------PCSSATEQTERDSATAYRMTVE 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 POEDAWASPGAYGMGGRYPWPSSAPSAPPGNLYM----TESTSPWP----SSGS-PQS 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 PSSCLWAEP---GMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSGSCPTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09416214
Patent No. 6413728
GENERAL INFORMATION:
APPLICANT: Gooddal, David V.
APPLICANT: Jiang, Yingping
TITLE OF INVENTION: Supressors of Death Domains
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBORGUGH
STATE: CALIFORNIA
                                                                                                                                  ZIP: 9401U
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PB PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          !XSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
TECHNOLOGY LAW GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 VLGTVLGTAIQGQIVGQA--DTPCFQDFNSS 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLDSQVQYSAEPQLYGNATSDHPNNQDQSSS 364
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/416,213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 35,627
REFERENCE/DOCKET NUMBER: T98-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/035,676
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
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3: SCIENCE & TER
75 DENISE DRIVE
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ISPVLGLSAAVWAKILSSFTDKELLAYAKAGAVAEEVLAAIRTVIAFGGQKKELERYNKN 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TRGCSQPERVKFT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 LTVFFSVLIGAFSVGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIK-- 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------GNLEFRNVHFSYP----SRKEVKILKGLNLKVQSGQTVALVGNS 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 VGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILILGV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------NSSPEEMVSVYH------FWTIVLAIAGMV--LYFIC----FKST 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 DTGLFTVLVL-----VQNPGWYCGIGTAGAXMVARIGKKTFLIGALLGTCGYLLFFWV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRNEFQNLLLLAIMLSATLTIPIW------QWFLTRFGKKTAVYVGISSAVPFLILVAL 304
                                                                                                                                                     LNTRLTDDVSKINEGIGDKI--GMFFQSMA-----TFFTGFIVGFTRGWKLTLVILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RENVVRIVAQPSLNIS----LQTLKRNRPLFMLCIGALCVLISTFAVSASSLF---YVLN
                                                                                51 MVVGTLAAIIHGAGLPLMMLVFGEMTDIFANAGNLEDLMSNITNRSDINDTGFFMNLEED
                                                                                                                                                                                                               RGLRLV-----MSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLGFRNEFQNLLLAIM
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                                                                                                                                                                                                                                                                                                                                                                             MESNLIITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFY----
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      67; Mismatches 148; Indels 131; Gaps
                                                                                                                             166 -TQKAYL---LAAGVIVCIYIICAVILILGVRE----QREPYEAQQSEPIAYF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 INMLVIMAPIVLILIGLILFK----MYPIDEERRRQNKKALQALRDEASS----
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19.0%; Pred. No. 0.059;
tive 59; Mismatches 169;
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APPLICATION NUMBER: US/07/447,976
FILING DATE: 08-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 119,102
FILING DATE: 10-NOV-1987
APPLICATION NUMBER: 264,586
FILING DATE: 31-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 19.00
The Conservative 71; Conservative 71; Conservative
      Conservative
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NUMBER OF SEQUENCES: 9
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      Matches 84;
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TITLE OF INVENTION: Methods and Reagents for Preparing and
TITLE OF INVENTION: Using Immunoligcal Agents Specific for P-glycoprotein
                                                                                                                                                             221 ISPVLGLSAAVWAKILSSFTDKELLAYAKAGAVAEEVLAAIRTVIAFGGOKKELERYNKN 280
                                                                                                                                                                                                                                                    331
MTRYAYYYSGIGAGVLVAAYIQVSFWCLAAGRQIHKIRKQFFHAIMRQEIGWFDVHDVGE 170
                                         RGLRLV-----MSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLGFRNEFQNLLLAIM 265
                                                                                                                                                                                                                                                                                                                             332 LTVFFSVLIGAFSVGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIK-- 389
                                                                                                                                                                                                                                                                                                                                                                                                                -----GNLEFRNVHFSYP----SRKEVKILKGLNLKVQSGQTVALVGNS 429
                                                                                                                                                                                                                                                                                         --VFFTKFASGVSLGISTLSLDF-----AGYQ------TRGCSQPERVKFT 397
                                                                                                                                                                                                                                                                                                                                                                         398 LNMLVTMAPIVLILLGILLFK----MYPIDEERRRQNKKALQALRDEASS------S 444
                                                                                171 LNTRLTDDVSKINEGIGDKI -- GMFFQSMA-----TFFTGFIVGFTRGWKLTLVILA
                                                                                                                                                                                                                                     MESNLIITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFY---
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                                                                                                                           LSAT -- LTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVAL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.
STREET: 300 South Wacker Drive, Seventh Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/316,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95,1121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/752,447
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. 6365357nan, Kevin E
RATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09316167
Patent No. 6365357
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-9808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mechetner, Eugene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1280 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430 GCGKSTTVQL 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           445 GCSETDSTEL 454
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 300 cc.
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
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310 FFWVSVWSLPVALVALAIASIGOGVTMTVMWALEADTVE-----YGEYLTGVRIEG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRNEFQNLLLAIMLSATLTI---PIW-----QWFLTRFGKKTAVYVG-ISSAVPFLI 300
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292 MKSCAVIVGLLVGCIVAAACGYFDRSGIDAAPVASFIWVKTFPLTIYAPLILPLLAVYMV 351
                                                                           352 IMMESIGDITATCDVSRLQVEGATFDSRIQGGVLGNGITCLLAGLCTITPMSVFAQNNGV 411
                                                                                                                  148 TVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILILGVREQREPYEAQQSEPI 207
                                                                                                                                                                                              AYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLGFRNEF-QNLLLAIML 266
                                                                                                                                                                                                                                                                           SATLTIPIW-QWFLTRFGKKTAVYVGISSAVPFLILVALMESNLIITYAVAVAAGISVAA 325
                                                                                                                                                                                                                                                                                                                AATL-VPDWFSYFFTYSGDNHAL-EGLLQAV------ELVMANGFAVTGFLGLLL 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: JEFFERSON, RICHARD A.
TITLE OF INVENTION: PLAANT PROMOTER A-GLUCURONIDASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168;
                                      100 SATEQTERDSATAYRMTVEVLGTVLGTAIQGQIVGQADT-
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Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/447,976
FILING DATE: 08-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 119,102
FILING DATE: 10-NOV-1987
APPLICATION NUMBER: 264,586
FILING DATE: 31-OCT-1988
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18.9%; Pre
tive 61;
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                                                                                                                                                       412 IALTPCANRKAG-----
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Best Local Similarity 18.99
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Patent No. 5268463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;SEQ ID NO:7:
; LENGTH: 457
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                                                                                                                                                                                                          APPLICANT: Guimaraes, M. Jorge
APPLICANT: Bazan, J. Fernando
APPLICANT: McClanahan, Terrill K.
APPLICANT: ACCIAnahan, Terrill K.
TITLE OF INVENTION: PURIFIED MAMMALIAN NUCLEOBASE PERMEASES;
TITLE OF FINVENTION: NUCLEIC ACIDS; ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 580
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LOCATION: 437..499
OTHER INFORMATION: /note= "Encompasses TM 9 and TM 10
OTHER INFORMATION: of Figure 4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATIS TYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 TSHTARPIGT --- CFSIASLKQWSR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,788
FILING DATE: 03-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,049
FILING DATE: 03-UUL-1996
CLASSIFICATION: 435
                                                                                                                                                       Sequence 12, Application US/08677049 Patent No. 5858707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 580 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 21.4%
nes 80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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OTHER INFORMATION:
OTHER INFORMATION:
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432 GKSTTVQL 439
                  SETDSTEL 454
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California
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Matches
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June 19, 2003, 17:48:07; Search time 25 Seconds (without alignments) 1982.349 Million cell updates/sec
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2384
1 MWLRWALSLPPSSCLWAEPG......DEASSSGCSETDSTELASIL 458
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                      OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

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	Description	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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ALIGNMENTS

RESULT 1 US-09-992-598-20

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Published_Applications_AA:*

Database :

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Sequence	GENERAL I	APPLICANT:	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	TITLE OF	TITLE OF	FILE REF	CURRENT	CURRENT	PRIOR AP	PRIOR FI		PRIOR FI	PRIOR AP			PRIOR FI
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APPLICANT:
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DR FILING DATE: 1998-07-02
DR APPLICATION NUMBER: 60/091978
DR FILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/091982
DR FILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/09182
DR APPLICATION NUMBER: 60/092182
DR FILING DATE: 1998-07-09
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Patent No. US20020177164A1
                             APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
                                                                APPLICATION NUMBER: 60/091626
APPLICATION NUMBER: 60/091544
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                                                                              FILING DATE: 1998-07-02
               1998-07-01
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Gerber, Hanspeter
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nes 458; Conservative
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APPLICANT: Ashkenazi, Avi J.
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Desnoyers, Luc
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Napier, Mary A.
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Watanabe, Colin K.
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A PETLING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089512
R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089514
JR FILING DATE: 1998-06-16
DR APPLICATION NUMBER: 60/089532
THING DATE: 1998-06-17
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R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088217
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R APPLICATION NUMBER: 60/086810
R RAPLICATION NUMBER: 60/086824
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R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089600
RR APPLICATION NUMBER: 60/089653
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R APPLICATION NUMBER: 60/089653
                                                 APPLICATION NUMBER: 66/088167
PILING DATE: 1998-06-04
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APPLICATION NUMBER: 66/088202
FILING DATE: 1998-06-05
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FILING DATE: 1998-06-18
PLICATION NUMBER: 60/088033
LING DATE: 1998-06-04
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APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-19
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R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/087106
R PILING DATE: 1998-05-28
R APPLICATION NUMBER: 60/087607
R PILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/049787
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APPLICATION NUMBER: 60/062250
FILING DATE: 1997-10-17
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NG DATE: 1998-02-25
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1998-06-02
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NG DATE: 1998-06-02
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FILLING DATE: 1998 -06-03
APPLICATION NUMBER: 60/088021
FILLING DATE: 1998 -06-04
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088029
FILING DATE: 1998-06-04
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Grimaldi,J.Christopher
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
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Ferrara, Napoleone
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Gerritsen, Mary E
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                                           GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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R APPLICATION NUMBER: 60/089538
R FILING DATE: 1998-06-17
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R FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/090445
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-16
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
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180 61 SGSCPTSHTARPIGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATATRWTVEVL 120 121 GTVLGTAIQGQIVGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCI 180 241 GNFVLFCTYTLGFRNEFQNLLLAIMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLI 300 9 9 SGSCPTSHTARPIGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVL GTVLGTAIQQQIVGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCI YIICAVILILGVREQREPYEAQOSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVE 241 GNFVLFCTYTLGFRNEFQNLLLAIMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLI LVALMESNLIITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYV FFTKFASGVSLGISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMY 1 MWLRWALSLPPSSCLWAEPGMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSS .; 0 PIDEERRRQNKKALQALRDEASSSGCSETDSTELASIL 458 100.0%; Score 2384; DB 9; 100.0%; Pred. No. 5.4e-185; ive 0; Mismatches 0; PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PILING DATE: 1998-06-25
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PRIOR PILING DATE: 1998-06-26
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PRIOR FILING DATE: 1998-06-26
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PRIOR PILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09163
PRIOR FILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09182
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09182 RESULT 6
US-09-990-436-20
Second Seco APPLICANT: Ashkenazi,Avi J.
APPLICANT: Baker,Kevin P.
APPLICANT: Botstein,David
APPLICANT: Eaton,Evic Query Match 100. Best Local Similarity 100. Matches 458; Conservative 301 361 361 121 421 421 유 ŏ g

420 420

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERENCE: P2730PIC53
CURRENT APPLICATION NUMBER: US/09/991,181
CURRENT APPLICATION NUMBER: 00/049787
PRIOR APPLICATION NUMBER: 00/049787
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 00/06570
PRIOR APPLICATION NUMBER: 00/065311
PRIOR PILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 00/065311
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-10-25
PRIOR PELING DATE: 1997-10-26
PRIOR PELING DATE: 1998-02-25
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PRIOR PELING DATE: 1998-05-20
PRIOR PLING DATE: 1998-05-20
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-03
301 LVALMESNLIITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYV 360
                                                Sequence 20, Application US/09991181 Publication No. US20020197615A1 GENERAL INFORMATION:
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Gurney,Austin L.
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Watanabe, Colin K.
Williams, P. Mickey.
Wood, William I.
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Stewart, Timothy A
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Fong, Sherman
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Goddard, Audrey
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Botstein, David
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                                                                   PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR APPLICATION NUMBER: 60/090540
PRIOR PILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/090567
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PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
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PRIOR APPLICATION NUMBER: 60/090691
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PRIOR FILING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-02
PRIOR PPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-02
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FILING DATE: 1998-07-07
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FILING DATE: 1998-07-09
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PRIOR APPLICATION NUMBER: 60/091633
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                                                   LICATION NUMBER: 60/090472
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R APPLICATION NUMBER: 60/088824
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088824
R APPLICATION NUMBER: 60/088826
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/08861
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/088861
R APPLICATION NUMBER: 60/08876
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/089105
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
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FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/089532

RELING DATE: 1998-06-17

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APPLICATION NUMBER: 60/089598
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PAPLICATION NUMBER: 60/089599
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ILING DATE: 1998-06-19
PPLICATION NUMBER: 60/090246
ILING DATE: 1998-06-22
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PPLICATION NUMBER: 60/090254
'ILING DATE: 1998-06-22
"PLICATION NUMBER: 60/090349
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089514
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PPLICATION NUMBER: 60/090355
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FILING DATE: 1998-06-24
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                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/989,734
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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R APPLICATION NUMBER: 60/087759
R FILING DATE: 1998-06-02
RR APPLICATION NUMBER: 60/087827
R APPLICATION NUMBER: 60/087827
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RIOR FILING DATE: 1997-11-24
RIOR PPLICATION NUMBER: 60/075945
RIOR FILING DATE: 1998-02-25
RIOR APPLICATION NUMBER: 60/078910
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088033
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APPLICATION NUMBER: 60/088212
FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/088028
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088202
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PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
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APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
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FILING DATE: 1998-06-02
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                                                                                               Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                        Roy, Margaret Ann
Stewart, Timothy A
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                                                                            rumas, Danie
                                                    Stewart,
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APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/089532
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APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/088326
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APPLICATION NUMBER: 60/088167
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FILING DATE: 1998-06-09
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APPLICATION NUMBER: 60/08858
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FILING DATE: 1998-06-12
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APPLICATION NUMBER: 60/088734
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61 SGSCPTSHTARPIGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVL 120 GTVLGTAIQGQIVGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCI 180 1 MWLRWALSLPPSSCLWAEPGMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSS 1 MMLRWALSLPPSSCLWAEPGMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSS ö Length 458; Indels Ouery Match 100.0%; Score 2384; DB 9; Best Local Similarity 100.0%; Pred. No. 5.4e-185; Matches 458; Conservative 0; Mismatches 0; APPLICATION DATE: 1998-07-02
APPLICATION NUMBER: 60/091544. APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090678 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090696 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/091360 APPLICATION NUMBER: 60/091978 FILING DATE: 1998-07-07 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090557 APPLICATION NUMBER: 60/090695 APPLICATION NUMBER: 60/090862 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/090863 APPLICATION NUMBER: 60/091519 APPLICATION NUMBER: 60/091626 APPLICATION NUMBER: 60/090431 APPLICATION NUMBER: 60/090444 60/090445 APPLICATION NUMBER: 60/090472 APPLICATION NUMBER: 60/090542 APPLICATION NUMBER: 60/090676 APPLICATION NUMBER: 60/090690 APPLICATION NUMBER: 60/090694 PLICATION NUMBER: 60/ LING DATE: 1998-06-23 FILING DATE: 1998-06-24 1998-06-25 1998-06-24 1998-06-24 1998-06-24 1998-06-24 1998-06-25 1998-06-25 LING DATE: 1998-06-25 1998-07-02 1998-06-24 998-06-24 LING DATE: 1998-07-01 1998-06-FILING DATE: 1998-06 APPLICATION NUMBER: FILING DATE: FILING DATE: LING DATE: LING DATE: LING DATE: LING DATE: 121 121

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R APPLICATION NUMBER: 60/090445
R FILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/090254
R FILING DATE: 1998-06-22
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R APPLICATION NUMBER: 60/090431
R FILING DATE: 1998-06-24
R R APPLICATION NUMBER: 60/090435
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APPLICATION NUMBER: 60/089948
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APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/089947
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APPLICATION NUMBER: 60/090246
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 67/090690
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-26
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APPLICATION NUMBER: 60/089801
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                                                                                                                                                                                                                                                                                                                                                                                   241 GNFVLFCTYTLGFRNEFQNLLLAIMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLI
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                                                                                                                                                1 MWLRWALSLPPSSCLWAEPGMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSS
                                                                                                                     Gaps
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0
                                                                                        Length 458
                                                                                                                   Indels
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; Pred. No. 5.4e-185;
0; Mismatches 0;
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Grimaldi,J.Christopher
Gurney,Austin L.
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100.0%;
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Williams, P. Mickey
Wood, William I.
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Ferrara, Napoleone
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Gerber, Hanspeter
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                                                                                     Query Match
Best Local Similarity 100.
Matches 458; Conservative
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITTLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/990,562
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APPLICATION NUMBER: 60/088202
FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/062250
FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/065186
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APPLICATION NUMBER: 60/088025
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PRIOR APPLICATION NUMBER: 60/049787
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APPLICATION NUMBER: 60/065311
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                                                                                                                          Goddard, Audrey
Godowski, Paul J.
Grimaldi, J.Christopher
                                                                                                                                                                                                                                                                                                                                                                                                    Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                          errara, Napoleone
                                                                                                                                                                                                                                                                                                                           Roy, Margaret Ann
Stewart, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               998-03-20
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                                                                        Gerber, Hanspeter
Gerritsen, Mary E.
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                                                                                                                                                                                                                                                                                                      Paoni, Nicholas F.
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                                                                                                                                                                                                   Gurney, Austin L.
                                                                                                                                                                                                                             Kljavin, Ivar J
                                                                                                                                                                                                                                                  Napier, Mary A.
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                            Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang, Zemin
                                                                                                                                                                                                                                                                               Pan,James
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100.0%; Pred. No. 5.4e-185;
ive 0; Mismatches 0;
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FILING DATE: 1998-07-09
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FILING DATE: 1998-07-02
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APPLICATION NUMBER: 60/091978
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APPLICATION NUMBER: 60/091982
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APPLICATION NUMBER: 60/090863
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FILING DATE: 1998-07-01
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APPLICATION NUMBER: 60/090695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 458; Conservative
                    FILING DATE: 1998-06
APPLICATION NUMBER:
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US-09-990-562-20
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Database :

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SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: BELONGS TO THE SODIUM:GALAGTOSIDE SYMPORTER FAMILY
                                                371 LGISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIV---LILLGLLLFKMYPIDEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning, sequence analysis, and characterization of the genes involved in isoprimeverose metabolism in Lactobacillus pentosus."; J. Bacteriol. 180:2312-2320(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chaillou S., Lokman B.C., Leer R.J., Posthuma C., Postma P.W., Pouwels P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chaillou S., Lokman B.C., Leer R.J., Posthuma C., Postma P.W., Pouwels P.H.;
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20.9%; Pred. No. 0.0042;
*ive 68; Mismatches 157; Indels
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
NCBL_TaxID-1589;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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TIGRFAMs; TIGR00792; gph; 1.
PROSITE; PS00872; NA_GALACTOSIDE_SYMP; 1.
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InterPro; IPR003662; sub_transporter.
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P96792:
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                                                            119 VLGTVLGTAIQGQIVGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIV
                                                                                                                                                                                                                                                           262 ---NFI----YWLGMQTRSQVTVYFFKYNMHDATLASFILGLQLVALLAVVITPWTAKRI
                                                                                                                                                                                                                                                                                                                                                            315 GKRNTMLMGMLLAIVGQLILWGGSKALNVPTITVGTIVGY-LGTGFVSGLIAVMLADSVD
                                                                                                  170 TIRQFMGT-LGATIISTIALPLVAYFGGGSTSS-----AHG-----WFMVALIMA
                                                                                                                                                                                                                                     239 VEGNFVLFCTYTLGFRNEFQ.........NLLLAIMLSATLTIPIWQWFLTRF
                                                                                                                                                                                                                                                                                                                        283 GKKTAVYVGISSA-VPFLILVALMESNLIITYAVAVAAGISVAAAFL--LPWSMLPDVID
                                                                                                                                                                                          214 VIAMVIFFIVFANTKERVQTVQSKKSIPIK--TSLKALKRNWPWVIVI--FI-----
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SEQUENCE FROM N.A.
STARAIN-KIZ / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blatther F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blatther F.R., Plunkett G. III, Bloch C.A., Royhew G.F.,
Kiley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence of Escherichia coli K-12.";
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Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 398 LNMLVTMAPIV --- LILLGLLLFKMYPI ---- DEERRRQNKKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glucuronide carrier protein (Glucuronide permease).
UIDB OR GUSB OR UIDP OR B1616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UIDB_ECOLI STANDARD; PRT; 457 AA. P30868; P77457; 01-JUL-1993 (Rel. 26, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-2001 (Rel. 40). Last annotation update) Glucuronide carrier protein (Glucuronide perme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=87041472; PubMed=3534890;
Jefferson R.A., Burgess S.M., Hirsh D.;
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PRELIMINARY SEQUENCE OF 1-112 FROM N.A.
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Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                   278 FLTRFGKKTAVYVGISSAVPFLILVALMESNLIITYAVAVAAGISVAAAFLLPWSMLPDV
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                                                                                                                                                                                               Gaps
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                                                                                                                                                                                            33;
                                                                                                                                                                     h 5.8%; Score 138.5; DB 1; Length 459; Similarity 18.9%; Pred. No. 0.013; 53; Conservative 70; Mismatches 167; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leenhouts R.K.J., Bolhuis A.A., Kok J.J., Venema G.G.;
Submitted (XXX-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE
SODIUM:GALACTOSIDE SYMPORTER FAMILY (SGF).
Hypothetical protein; Transport; Transmembrane; Symport;
                                                                                                                                                   B807795C3276E1E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Raffinose carrier protein (Raffinose permease).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.8%; Score 100,
19.8%; Pred. No. 0.021;
**ive 61; Mismatches 168; Indels
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(Rel. 37, Last sequence update)
(Rel. 41, Last annotation update)
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PROSITE; PS00872; NA_GALACTOSIDE_SYMP; 1.
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or send an email to license@isb-sib.ch)
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InterPro; IPR001127; PTS_EIIA.
Pfam; PF00358; PTS_EIIA.1; 1.
PTODOM; PD002243; PTS_EIIA; 1.
TIGRPAMS; TIGR00792; gph; 1.
TIGRPAMS; TIGR00830; PTBA; 1.
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                                            EMBL; Z32771; CAA83664.1; -. EMBL; L32093; AAA25563.1; -. HSSP; P20166; 1GPR.
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-----MLANIAHDMVVCVQQPMF--TE-MEGASYRY-----SGAGVGYQVASVVGGGF-- 395
                  272 IPIWQWFLTRFGKK----TAVYVGISSAVPFLILVALMESNLIITYAVAVAAGISVAAAF 327
                                                                LLPWSMLPDVIDDF--HLKQPHFHGTEPIFFSFYVFFTKFASGVSLGISTLSLDFAGYQT
                                      303 IPCFAWLADRFGRRRVYITGTLIGTLSAFPFFMALEAQSIFWIVFFSI--
                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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cocene: SG13346; yagG.
InterPro; IPR001927; Na/Gal_symp.
TIGREAMS; TIGR00792; gph; 1.
                                                                                                                                                                                                    P75683; P71292;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seque
16-OCT-2001 (Rel. 40; Last annot.
Hypothetical symporter yagg.
YAGG OR B0270.
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TRANSMEM
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                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 AIOGFAVG-----GEWGGAALLSVESAPKNKKAFYSSGVQVGYGVGLLLSTGLVSLIS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 AIQGQIVGQADTPCFQDFNSSTVAS-QSANHTHGTTSHRETQKAY----LLAAGVIVCIY 181
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                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakames S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T., A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95;
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B7FFBBD5AFDAE8CC CRC64;
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CYTOPLASMIC (POTENTIAL).
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PERIPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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PERIPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                         Pfam, PF00083; sugar_tr; 1.
TIGRRAMS; TIGR00883; 2A0106; 1.
PROSITE; PS00216; SUGAR_TRANSPORT_1;
PROSITE; PS00217; SUGAR_TRANSPORT_2;
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EMBL; AE000290; AAC75045.1; -.
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                                                                                               DNA Res. 3:379-392(1996).
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438 AA;
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Best Local Similarity
Matches 78; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=KIZ. / MG1657.
STRAIN=KIZ. / MG1657.
PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Greegor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
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Schramm S., Duccan M., Allen E., Araujo R., Aparicio A., Chung E.,
Schramm S., Boccarspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
386 RGCSQPERVKFTLNMLVTM-----APIVLILLGLLLFKMYPI---DEER 426
                                                       PROSITE; PS00872; NA_GALACTOSIDE_SYMP; 1.
Hypothetical protein; Transport; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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485 AA;
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185
238
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303
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@lsb-sib.ch).
                                                                                                                               12;
                                                                                                                                                  167 QKAYLLAAGVIVCIYIICAV-----ILILGVREQREPYEAQQSEPIAYFRGLRLVMSHG 220
                                                                                                                                                                                                                                             279 LTRFGK-----KTAVYVGISSAVPF-----LILVALMESNLIITYAVAVAAGISVAAAF 327
                                                                                                                                                                                                                       PPSTLTLTYMLATLPGFIGSYLGAMMYFVTYYLGSASYFMWMLAAHILGKAAGSLLAKRL 111
                                                                                                                                                                                               PYIKLITGFLFTSLAFMLVE - GNFVLFCTYTLGFRNEFQNLLLAIMLSATLTIPIWQWF
                                                                                                                                                                                                                                                                    112 TRNFNKVOIFGYCAVLAGVLSIALFFAPKSVFVLVPL-----TFIISTL----YQATT
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                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                          388 CSQPERVKFTLNMLVTMAPIVLILLGLLF---KMYPIDEERRRQ-NKKALQAL 437
                                                                                                                                                                                                                                                                                                                                                        STRAIN=K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDILNE-93347969; PubMed-8346018;
Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
"Analysis of the Escherichia coli genome. III. DNA sequence of the region from 87.2 to 89.2 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                     Score 112; DB 1; Length 27
Pred. No. 0.5;
1; Mismatches 122; Indels
                                             InterPro; IPR001927; Na/Gal_symp.
PROSTTE; PS00872; Na_GALACTOSIDE_SYMP; FALSE_NEG.
Hypothetical protein.
SEQUENCE 272 AA; 29955 WW; C7C753B416F14AB6 CRC64;
                                                                                                                                                                  (Rel. 40, Last sequence update) (Rel. 40, Last annotation update)
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P32136; P76774;
01-0CT-1993 (Rel. 27, Created)
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                                  EMBL; M87280; AAA64975.1;
                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 TGIRAEGSVYTGYTFFRKISAALAGFLPGIMLTQIGY-VPNIAQSDATLQGLRQLIFIWP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 LWAVGDILNYFWGSNSFTFVMFSCVAFFGTAFVNSLNWALVPDTVD------YGEWK
    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 PIGTCFSIA-----SLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 PVKTTIATALFMMFGLSYSLMNCSYGAMIP-----AITKNPNERAQLAAYRQGGATIGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 VLGTAIQGQIVGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 LICTV------AFIPLQSLFSDSTVGYACA-------ALMFSIGGF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ICAVILILGVREQREPY - - EAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 GNFVLFCTYTLGFRNEFQNLL-----LAIMLSATLTIPIWQWFLTRFGKKTAVYVGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257 AIQVYYTQYVL---NDI-NLLSWMGFFSMGCILIGVLLVPL---TVKCFGKKQVYLAGMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 SAVPFLILVALMESNLIITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----TEPIFFSFYVFFTKFASGVSLGISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
  is in
                                                                                                                                                                                                                                                    PROSITE; PSO0872; NA_ĜALACTOSIDE_SYMP; 1.
Hypothetical protein; Transport; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.6%; Score 110; DB 1; Length 485;
    as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FB53C0CE17756500 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   407 IVL-ILLGLLFKMYPIDEER-----RRQNKK 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 420 CALAIIAALTMGFFYTLNEKRFALIIEEINQRKNKE 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172;
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non-profit institutions as long
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                                                                                                           EMBL; L19201; AAB03009.1; ALT_FRAME.
EMBL; AE000463; AAC76873.1; ALT_INIT
PIR; S40820; S40820.
ECOGENE; EG11841; Yiho.
InterPro; IPR001927; Na/Gal_Symp.
TIGREAMS; TIGR00792; gph; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53817 MW;
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TRANSMEM
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                                                                                                                                                                                               Runst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Kunst F., Ogasawara N., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Bruschi C. V., Caldell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C. V., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Brouillet S., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T.,
RA Britz C., Fulita M., Fulita Y., Funas S., Galizzi A., Galleron N.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappei S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Murita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
A Nobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Modina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle B., Rapoport G., Rey M., Sacott A.M.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Schleich S., Schoeter R., Kose M., Saror S.J., Serror P., Shin B.S.,
Sakiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,
A Takeuchi M., Tamakoshi A., Tanaka T., Tarkahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanama T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanama T., Vanamoto K., Yasumoto K., Yata K.,
Winters P., Wibpat A., Yamamoto H., Wambut F., Voshikawa H., Danchin A.,
The complete genome sequence of the Gram-positive bacterium Bacillus
F. The Complete Genome sequence of the Gram-positive bacterium Bacillus
                          MEDLINE-98240225; PubMed-9579062;
Rivolta C., Soldo B., Lazarevic V., Joris B., Mauel C., Karamata D.;
"A 35.7 kb DNA fragment from the Bacillus subtilis chromosome
containing a putative 12.3 kb operon involved in hexuronate catabolism
and a perfectly symmetrical hypothetical catabolite-responsive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein (By similarity). SIMILARITY: BELONGS TO THE PHTHALATE PERMEASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       !- FUNCTION: ALDOHEXURONATE TRANSPORT SYSTEM.
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InterPro; IPR003662; sub_transporter.
                                                                                                                                                                                        MEDLINE-98044033; PubMed-9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00083; sugar_tr; 1.
TIGRFAMS; TIGR00893; 2A0114; 1.
                                                                                                            element.";
Microbiology 144:877-884(1998).
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SubtiList; BG13210; exuT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997)
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102
161
183
183
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SEQUENCE FROM N.A.
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278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 ISVAAAFL-----LPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLGIST 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
                                                                                                                                                                                                                                                                                                                                      108 DSATAYRMIVEVLGIVLGTALGGOIVGQADIPCFQDFNSSIVASQSANHIHGITSHRETQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 -SWKVSFVLIMIIGLIWAVLWFKFVKE--KPQETIKEAP-----AIKAETSPGEKIPLTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 LGFIGLAAGGFVSDYVYKKTA-RKGVLFSRKVVLVTCLFSSAVLIGFAGLVATTAGAVTL
                                                                                                                                                                                                                            62 GSCPTSHTARPIGTCFSIASLKQWSRVSMFPTRL-----SPCSSATEQ-----TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 YIKLITGFLFTSLAFMLVEGNFVLFCTYTLGFRNEFQNLLL---AIMLSATLTIPIWQWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 YLKQKT-VLFTAFAFFAY--NYILFF-----FLTWFPSYLVDERGLSVESMSVITVIPWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 LTRFG-----KKTAVYVGISSAVPFLILVALMESNLIITYA--VAVAAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 KAYLLAAGVIVCIYIICAVILILGVREQREPYEAQOSEPIAYFRGLRLVMSHGP-----
                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Human).
etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;
Science 283:1852-1852(1999).
-!- FUNCTION: INHIBITS THE CHAPERONE ACTIVITY OF HSP70/HSC70 BY
PROMOTING SUBSTRATE RELEASE.
-!- SUBGUNI: BIRDS TO THE ATPASE DOMAIN OF HSP70/HSC CHAPERONES.
                                                                                                                                                                       Indels 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAG4_HUMAN STANDARD; PRT; 457 AA.
095429; 095818;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
BAG-family molecular chaperone regulator-4 (Silencer of death
                                                                                                                  Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takayama S., Xie Z., Reed J.C.; "An evolutionarily conserved family of Hsp70/Hsc70 molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                              131 ASV----IGVTNSGTPLGGAISGPIVGMI-----AVAF---
                                                          C2E291AF347F7EDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               376 LSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLF 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----NTAGIIGPALTGFIVDQTGTFSGAFLLAGGLAVF 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 VALSVFFLYLTGAIYWAVIQDVVDQNNV-----GSVGGFMHFLA-
                                                                                                                  DB 1;
                                                                                                                                       21.9%; Pred. No. 1.2;
tive 58; Mismatches 133;
                                                                                                               4.6%; score 109.5;
     POTENTIAL.
                                POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99091615; Pubmed=9873016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chaperone regulators.";
J. Biol. Chem. 274:781-786(1999).
                                                          45313 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 283:543-546(1999).
                                                                                                                                                                       Conservative
.356 3
381 4
422 AA;
                                                                                                                                             Similarity
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                                                                                                                                                                       88;
                                PRANSMEM
                                                          SEQUENCE
                                                                                                               Query Match
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                                                                                                                                                Sest Local
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OM protein - protein search, using sw model

Run on:

June 19, 2003, 17:45:42; Search time 19 Seconds (without alignments) 2317.346 Million cell updates/sec

US-09-941-992-20 2384 1 MWLRWALSLPPSSCIWAEPG......DEASSSGCSETDSTELASIL 458 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	~	sugar, proton sympo		sodium-qalactoside	permease of the Na	glucuronide permea				raffinose carrier	H+-symporter homol	Sodium, galactoside	shikimate transpor	probable transport		probable permease			sodium-qalactoside	xyloside transport							probable permease	iron(III) ABC tran
SUMMARIES	OI.	AB2269	875696	E97320	н69788	H87465	D96985	C90919	н85767	B64918	D69852	S44253	A69888	AC0122	G64962	н85822	B90976	B91186	A86033	F64752	D87624	B86813	B97324	C75483	AE0507	F91228	S52977	S55316	E86075	D82302
	DB	7	7	~	7	7	7	7	7	7	~	~	7	7	7	7	7	7	7	7	7	7	7	C)	~	~	~	7	~	7
	Length	487	544	445	463	514	449	457	457	457	459	4	463	477	438	438	438	466	466	460	463	490	458	1136	457	467	272	317	469	541
æ	Query	12.9	9.3	6.5	6.4	6.2	6.1	6.1	6.1	9.0	5.8	5.8	5.6	5.6	5.5	5.4	5.3	5.3	5.3	5.3	5.3	5.0	4.9	4.9	4.7	4.7	4.7	4.7	4.7	4.7
	Score	308.5	221.5	154	153.5	147	145	144.5		143.5	138.5	138	133	132.5	131.5	128.5	127.5	127.5		126.5	126	119	118	117.5	113	113	112	112	112	112
	Result No.	7	7	m	4	S	9	7	80	O	10	11	12	13	14	. 15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

qq δλ

hypothetical prote	tetracycline resis	probable permease	genome polyprotein	hexuronate transpo	cation efflux syst	tetracycline resis	gastric mucin (clo	cationic amino aci	hypothetical prote	transport system p	hypothetical prote	probable amino aci	hypothetical prote	multidrug resistan	transport system p
555894	D71851	S40820	GNWVMV	A69853	н84126	E64665	147141	E69471	AF2115	AE1354	A89880	AI0701	T16084	DVHU1	AF1724
7	~	~	Н	-	N	~	~	7	7	~	~	~	~		a
374	386	487	3434	422	1093	386	528	531	387	402	265	447	501	1280	402
4.7	4.6	4.6	4.6	4.6	4.6	4.6	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4 . 4
111	110	110	110	109.5	109.5	108.5	108	108	107.5	107.5	107	106.5	106.5	106.5	106
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 AB2269 hypothetical protein alr3705 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AB2269 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, DNA Res. 8, 205-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyano A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Status: preliminary A;Nolecule type: DNA A;Residues: 1-487 <kurs 7120="" a;cross-references:="" a;experimental="" a;gene:="" alr3705<="" c;genetics:="" gb:ba000019;="" gspdb:gn00="" pcc="" pid:g17132839;="" pidn:bab75404.1;="" source:="" strain="" th=""><th>RESULT 1 AB2269 Althorical protein alr3705 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AB2269 B:Xaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata N.; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Accession: AB2269 A;Access</th></kurs>	RESULT 1 AB2269 Althorical protein alr3705 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AB2269 B:Xaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata N.; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Accession: AB2269 A;Access
 Query Match 12.9%; Scor Best Local Similarity 25.5%; Pred Matches 92; Conservative 68; M	<pre>i; Score 308.5; DB 2; Length 487; i; Pred. No. 1e-15; 68; Mismatches 148; Indels 53; Gaps 10;</pre>
 QY 93 TRLSPCSSATEQTERDSATAYRWT : : : : 151 TALTP-ELTQDYDERTSLNSFRFA	93 TRLSPCSSATEQTERDSATAYRMTVEVLGTVLGTALQGQIVGQADTPCFQDFNSSTVASQ 152
 Qy 153 SANḤTHGTTSHRETQKAYLLAAGV : : : : : : : :	153 SANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILLILGVREQREPYEAQQSEPI 207 :
 Qy 208 AYFRGLRLVMSHGPYIKLITGFLFTS : :: :: : : Db 243 PFFEQLKIVFSNRPFLFVIGIYLFSW	208 AYFRGLRIVMSHGPYIKLITGFLFFSLAFMLVEGNFVLFCTYTLGF-RNEFQNLLLAIML 266
 Qy 267 SATLTIPIWQWFLTRFGKKTAVYV : : : : :	267 SATLTIPINQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLIITYAVAVAAGIS 322
 Qy 323 VAAAFLLPWSMLPDVIDDFHLK 560 VSTAXLVPWSMIPDVIELDELQTG	323 VAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLGISTLSLDF 380
Qy 381 AGYQTRGCSQPERVKFTL 11 11 11 1 1 1 1 1 1	381 AGYOTRGCSOPERVKFTLAMLVTMAPIVLILLGLLLFKMYPIDEERRRONKKAL 434 : :

ж.

Zeng, Q.; Gibson,

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permease of the Na+, galactoside symporter family [imported] - Clostridium acetobutyl C; Species: Clostridium acetobutylicum C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C; Accession: D96985
                                                                                                                                                                                        A; Residues: 1-449 <KUR>
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Matches 75; Conserv
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                                                                                                                                                            A; Status: preliminary A; Molecule type: DNA
                                                                                                                                               A; Accession: D96985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 MGWFIVILLPITVLLAVMTVKEPAAPPQHGKTGLKQYWRLLMR--PSVQRL---LFADLL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FMLVEG----NFVLFCTYTLGF-RNEFQNLLLAIMLSATLTIPIWQWFLTRFGKKTAVYV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GISSAVPFLIL----VALMESNLIITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQP 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344 ---AAVVYAFVQVGAVFMPAGSSVMGMLLLVLAGLPYSAAPVLVRSMMADIGDEERLES- 399
                                                                                                                                                            313 YAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHG·-TEPIFFSFYVFFTKFASGVS 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HFHGTEPIFFSFYVFFTKFASGVSLGIST-LSLDFAGYQTRGCSQPERVKFTLNMLVTMA 405
                                                           --- DOAFGFOMTALIYAAVSIVLNLFSFFTVRERIQ 225
                                                                                                       | : :: | : : | : : | : | : | | : | | 226 PKKRKKQ---GIKKTLSVLFKNKPLLMLISSFLAFAIGFNIKLSTWVYFTYNVNHK-EF 281
                                                                                                                                            ----QNLLLAIMLSATLTIPIWQWFLTRFGKKTAVYVGIS-SAVPFLILVALMESNLIIT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400 ---GVDKTGLLYAIVTGTVKLGYALAVAVFIALGWMGFDPK-VSTPEGDAALIGM-YAIA 454
                               TPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILLLGVREQRE 197
                                                                                                                                                                                                                    : |:| | | | :: | | | 339 FIWLFASGFFTTPLNTLAWGMVADCVDYAEWKT----GIRADGVVISSMSFINKLGVALA 394
                                                                                                                                                                                                                                                                             198 PYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLGFRNEF
                                                                                                                                                                                                                                                           LGISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIV--'LILLGLLLFKMYPIDEER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              406 PIVLILLGLLFKMYPIDEERRRQNKKALQALRDEA---SSSGCSETDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 SSTVASQSANHTHGTTSHRETQKAY--LLAAGVIVCIYIIC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 79; Conserv
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Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: C90919
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                           Solvent-Producing Bacterium
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                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE001437; PIDN:AAK78671.1; PID:g15023572; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-457 <HAY>
A;CROSTreferences: GB:BA000007; PIDN:BAB35746.1; PID:g13361790; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRWTVEVLGTVLGTAIQGQI 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || : | | | | | | | 347 IDYGEWRT----GTRREGITYSVFNFARKLAQSIAGLLSGWGLGFVGY-VANKKQSAHAL 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 YLLAAGVIVCIYIICAVILILGVREQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 LFTSLAFMLVEGNFVLFCTYTLGFRNEFONLLLAIMLS-----ATLTIPIWOWFLTRFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKTAVYVGISSAVPFLILVALMESNLII ----TYAVAVAG-ISVAAAFLLPWSMLPDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 449;
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.;
J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4833, 483, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solve
A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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larity 19.8%; Pred. No. 0.0023;
Conservative 62; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.1%; Score 145; DB 2; I
Best Local Similarity 23.2%; Pred. No. 0.002;
Matches 63; Conservative 49; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396 FTLNMLVTMAP-IVLILLGLLLFKMYPIDEER 426
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C, Superfamily: melibiose carrier protein
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C;Superfamily: melibiose carrier protein
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us-09-941-992-20.rpr

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Page

13;

66; Gaps

Indels Length

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C;Superfamily: phosphotransferase system glucose-specific enzyme II, factor III homol C;Keywords: sugar transport; transmembrane protein F;485-639/Domain: phosphotransferase system glucose-specific enzyme II, factor III ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILI-----L 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGKPKSFSILSIINIFLGLI--ATSLFPV----LSKKFSRKGVFAG---CLVFMLGGIAI 332
                                                                                                                                                                                                                                                                                             77 FSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVLGTAIQGQIVGQA 136
                                                                                                                                                                                                                                                                                                                                                              YSFKDVGFW---SMLP----SLTTDSREREKTATFAR------LGSTIGGGLVGVL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGFRNEFQ----NLLLAIMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLI----L 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 VALMESNLIITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVF 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 FTIAGSNLWLVLLAATWFGFPQQMVFLVVLMVITDSVEYGQLKLG--HRDESLALSVRPL 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 FTKFASGVSLG----ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLF 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVREQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYT
                                                                                                                                                          Query Match 5.8%; Score 138; DB 2; L
Best Local Similarity 19.8%; Pred. No. 0.01;
Matches 73; Conservative 61; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KMYPIDEE 425
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A: Residues: 1-463 <KUN>
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                 Cyccession: D69852

R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carrer, N.M.; Chc
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucell
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Scanlon,
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scanlon,
A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama,
T.; Winters; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A; Reference number: A69580; MUID:988044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:299110; GB:AL009126; NID:g2633472; PIDN:CAB13088.1; PID:g2633585
A;Experimental source: strain.168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Taffinose carrier protein - Pediococcus pentosaceus
NiAlternate names: raffinose permease; raffinose transport protein
Cipceies: Pediococcus pentosaceus
Cipceis: Pediococcus pentosaceus
Cipcession: 84423;
Ricession: 84423;
Ricenhouts, K.K.J.; Bolhuis, A.A.; Kok, J.J.; Venema, G.G.
Ricenhouts, K.K.J.; Bolhuis, A.A.; Kok, J.J.; Venema, G.G.
Aibernited to the EMBL Data Library, April 1994
Aibertition: The sucrose and raffinose operons of Pediococcus pentosaceus PPEL.O.
Aireference number: 84425
Airession: 844253
Airession: 844253
Airession: 844253
Airession: 844253
Airession: 844253
Airession: 844253
Cipcestences: EMBL: 232771; NID:9493728; PIDN:CAA83664.1; PID:9475964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; nucleic acid sequence not shown; translation not shown 'A;Molecule type: DNA A;Residues: 1-459 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLGFRNEFQNLLLAIMLSATLTIPIWQW 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLTRFGKKTAVYVGISSAVPFLILVALMESNLIITYAVAVAAGISVAAAFLLPWSMLPDV 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLGISTLSLDFAGYQTRGCSQPERVKFT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 IDYGEWKSG--ERKEATTYSLFNFSRKLAQSLSGFLSGIGLGIIGY-VPNAVQTAQALIG 417
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGTTSHRETQKAYLLAAGVIVCIYIICAVILLLGVREQREPYEAQQSEPIAYFRGLRLVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 SSATEQIE-RDSATAYRMIVEVLGIVLGTAIQGQIVGQADIPCFQDFNSSIVASQSANHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GYPVVMGLFAALGVFWFYICYRNCKERIIISEAPK-EKLTLSSVVKTFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.8%; Score 138.5; DB 2; Length 459; 18.9%; Pred. No. 0.0064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | : : | : : | : : | : : : | IXALLILYPAIALAMFIIGFLYKLTDQQHAQ 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: melibiose carrier protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local
Matches 6
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H-Symporter homolog ynad - Bacillus subtilis
C;Species: Bacillus subtility
C
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A; Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
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22.8%; Pred. No. 0.017;
tive 65; Mismatches 138; Indels 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: melibiose carrier protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.6%
Best Local Similarity 22.8%
Matches 84; Conservative
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A; Residues: 1-438 CSTO>
A; Cross-references: GB:AE005174; NID:g12516157; PIDN:AAG57044.1; GSPDB:GN00145; UWGP:Z31
A; Experimental source: strain 0157:H7, substrain EDL933
C; Genetics:
A; Gene: shiA
C; Superfamily: citrate utilization determinant
                                                                                                                                                                                                                                                                                                                                                 probable transport protein, shikimate shiA [imported] - Escherichia coli (strain 0157:H7
C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D.J.; Mayhew
K.; Apodaca,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 MMTTDEQFLSWGWRIPPLESIVLVLGALWVRNGMEESAEFPQQQYNQAAKKRIPVIEAL 245
                                                                                              328 LLPWSMLPDVIDDF--HLKQPHFHGTEPIFFSFYVFFTKFASGVSLGISTLSLDFAGYQT 385
                                                                                                                        133 AIQGFAVG-----GEWGGAALLSVESAPKNKKAFYSSGVQVGYGVGLLLSTGLVSLIS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 I------ICAVILILGV-----REQREPYEAQQSEPIAYFRGLRLV--- 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 MSH-GPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLGFRNE-FONLLLAIMLSATLTIPI 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 LRHPGAFLKIIALRLCELLTMYIVTAFALNYSTQNMGLPRELFLNIGLLVGGLSCLTIPC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 WQWFLTRFGKK----TAVYVGISSAVPFLILVALMESNLIITYAVAVAAGISVAAAFLLP 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331 WSMLPDVIDDF--HLKQPHFHGTEPIFFSFYVFFTKFASGVSLGISTLSLDFAGYQTRGC 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272 IPIWQWFLTRFGKK----TAVYVGISSAVPFLILVALMESNLIITYAVAVAAGISVAAAF 327
                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C; Accession: H85822
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, 11ler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 AIQGQIVGQADTPCFQDFNSSTVAS-QSANHTHGTTSHRETQKAY----LLAAGVIVCIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                              || : | |||: | |||: | 303 IPCFAWLADRFGRRRYYITGTLIGTLSAFPFFWALEAQSIFWIVFFSI-----
                                                                                                                                                                                             386 RGCSQPERVKFTLNMLVTM-----APIVLILLGLLLFKMYPI---DEER 426
                                                                                                                                                                                                                           89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.4%; Score 128.5; DB 2; Length 438; Best Local Similarity 21.6%; Pred. No. 0.035; Matches 75; Conservative 58; Mismatches 125; Indels 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389 SQPERVKFTLNMLVTM-----APIVLILLGLLLFKMYPI---DEER 426
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A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                           396
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H85822
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O8tmg4 methanosarc
Q9k6b3 bacillus ha
Q8s5v1 oryza sativ
O25780 helicobacte
                                                                            09cfh0 lactococcus
097dm2 clostridium
09rwc9 deinococcus
08rs913 salmonella
08x8f0 escherichia
                                                                                                                                     09hed4 neurospora
029070 sus scrofa
095044 spitzallomyc
09kub4 vibrio chol
P70939 bacteroides
                                                                                                                                                                                                                     092k50 helicobacte
09q9f7 murray vall
                                                                                                                                                                                                                                                                                                     029071 sus scrofa
028500 archaeoglob
Q8yu77 anabaena sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8rim8 fusobacteri
046605 canis famil
                                                                                                                                                                                                                                                                                            Q988c1 rhizobium 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 QADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILILGVRE 194
 Q8r7f4 thermoanaer
                     09x425 lactococcus
09rav6 lactococcus
09rav9 lactococcus
                                                                                                                                                                                               Q8zrzl salmonella
Q9zb18 lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 TCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVLGTAIQGQIVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Qin W.X., Zhao X.T.,
Wan D.F., Gu J.R.,
"Novel human cDNA clones with function of inhibiting cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Similar to RIKEN CDNA 1700018018 gene (Hypothetical 58.6 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases EMBL; BC011587; AAH11587.1; -. EMBL; AF289609; AAL55793.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 530 AA; 58623 MW; 3B6978F4EA92C763 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.2%; Score 1816; DB 4;
94.3%; Pred. No. 1.2e-134;
ive 5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                         530 AA
                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                           Q9RAY9
Q8RIM8
Q46605
Q9CFH0
Q97DM2
Q9RWC9
Q8Z9N3
            Q9A413
Q9X425
Q9RAV6
                                                                                                                                     Q9HED4
Q29070
Q950R4
Q9KUB4
P70939
                                                                                                                                                                                              Q82R21
Q92B18
                                                                                                                                                                                                                     Q9ZK50
Q9Q9F7
Q8TMG4
Q9K6B3
Q8S5V1
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Matches 362; Conservative
434
463
494
494
494
489
1280
490
458
                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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386
3434
                                                                                                                                                                                                                                            506
1093
537
386
400
528
531
387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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Q96F59
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084947 anabaena sp

081813 thermoanaer

087813 thermoanaer

087813 clostridium

09746 caulobacter

0916 clostridium

08xmC0 clostridium

08xmC0 clostridium

08xmC0 are specification

08xmC0 secherichia

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                                                                                            (without alignments)
2696.274 Million cell updates/sec
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2384
1 WWLRWALSLPPSSCLWAEPG......DEASSSGCSETDSTELASIL
                                                                            June 19, 2003, 17:45:17; Search time 35 Seconds
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                          671580 seqs, 206047115 residues
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                                                       protein search, using sw model
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09A7H5
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08XK73
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Q8X4U5
Q8XDK7
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Q8YQV7
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
sp_unclassified:*
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sp_mammal:*
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Maximum Match 100%
Listing first 45 su
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sp_bacteriap:*
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sp_bacteria:*
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Match 1
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Perfect score:
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01-JUN-2002
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                          RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 TALTP-ELTODYDERTSLNSFRFAFSIGGSILSLIL-------SKVVLSL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 AYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLGF-RNEFQNLLLAIML 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 TALLMLFVWTALSKKIGKKLVYFLGMSS---WIIAAAGLFFLQPGQIGLMYVMAIMAGVG 359
267 SATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVA----LMESNLIITYAVAVAAGIS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 AGY-----QTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRRQNKKAL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILILGVREQREPYEA-----QQSEPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 VAAAFLLPWSMLPDVI--DDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLGISTLSLDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.9%; Score 308.5; DB 16; Length 25.5%; Pred. No. 3.3e-16; Live 68; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
NCBI_TaxID=103690;
                                                                                                                                       LFKMYPIDEERRRQNKKALQALRDEASSSGCSETDSTELASIL 458
                                                                                                                                                              (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
                                                                                                                                                                                                                                                                              487
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Hypothetical protein Alr3705.
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                                                                                                                                                                                                                                                                              PRELIMINARY;
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01-MAR-2002 (
01-MAR-2002 (
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108 YOV7
100 YOV7
100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLTIPIWQWFLTRFGKKTAVYVGISSAVPFLILV---ALMESNLIITYAVAVAAGISVAA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 LTAFKYVFLNKAFLPFVVGGFFAKFLLTSVPAAIPFFTKYVLRIPEKEVSLLLGSIFVTA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 IPMMLVWSKITKKFGSRKAMFLSIG----FLILVFPAYFFVNTFVETLIVSVIFGALLAG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 AFILLPWSMLPDVIDD----FHLKQPHFHGTEPIFFSFYVFFTKFASGVSLGISTLSLDFA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 VVMLLDVMLAEVIDEDTKNTGMKR---EGMYTGVFGFIIRFGYSLQGIVIG---GILKLS 408
                                                                                                                                                                         Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 GWNVLGIIFGT-----LIAIGFFIAFY------GCEEKKN----IKIPSIPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 FRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLGFRNEFQNLLL-AIMLSA
                                                                                                                                                                                                                                                                                                               DECUENCE FOUR WAS.

STRAIN-MB4T J JCM11007.

MEDLINE-21992816; PubMed=11997336;

Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J. Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling Tan H., Chen R., Wang J., Yu J., Yang H.;

"A complete sequence of T. tengcongensis genome.";

Genome Res. 12:689-700(2002).

EMBL; AE013144; AAM25111.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               382 GYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRRQN 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length 455;
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Bacteria; Firmloutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
NCBI_TaxID=1502;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             455 AA; 51339 MW; ED9CD6BB01AF4D65 CRC64;
                                                    01-JUN-2002 (TrEMBLrel. 21, Last sequence update) Na+/melibiose symporter and related transporters. MELB OR TTE1932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.1%; Score 169.5; DB 16; Best Local Similarity 21.8%; Pred. No. 2.6e-05; Matches 76; Conservative 52; Mismatches 154;
455 AA.
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21,
PRELIMINARY;
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STRAIN=13 / TYPE A;
Pubmed=11792842;
                                                                                                                                                                                                                                                   NCBI_TaxID=119072;
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Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

EMBL; AP003188; BAB80475.1; -
InterPro; IPR001927; Na/Gal_symp.

TIGRFAMS; TIGRO0792; ppi; 1.
Sugar transport; Complete proteome.
SEQUENCE 454 AA; 49661 MW; 9EDB58F22755A90E CRC64;
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Last sequence update)
Last annotation update)
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Last annotation update)
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0.9%; Pred. No. 0.0024;
ve 65; Mismatches 138;
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                                                         396 FTLNMLVTMAP-IVLILLGLLLFKMYPIDEER
                                                                                                                                                                                             454
                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                       Probable sugar transport protein. GUTA OR CPE0769.
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nes 64; Conservative
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STRAIN=13 / TYPE A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=13 / TYPE
PubMed=11792842;
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01-MAR-2002
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                                                                                                                                                                       236 FMLVEG----NFVLFCTYTLGF-RNEFQNLLLAIMLSATLTIPIWQWFLTRFGKKTAVYV
                                                                                                                                                                                                             284 MGLAPGIAGTLFLFFFERIKGFDKTQAGVLLLVYFLAALAGAPLWPMLAKKLGKHKALVV
                                                                                                                                                                                                                                                 GISSAVPFLIL----VALMESNLITTYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQP
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STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325; Pubmed-11466286;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

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"Bacterium IS3:4823-4838(2001).

"BME, AR007584; AAR7667.1.;

InterPro: IPR001927; Na/Gal_Symp.
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Clostridiales; Clostridiaceae; Clostridium.
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Pred, No. 0.0022;
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                   SSTVASQSANHTHGTTSHRETQKAY -- LLAAGVIVCIYIIC
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Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
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MEDLINE=21470413; PubMed=11586360;
Parkhill J., Waren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamiln N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Fersinia pestis, the causative agent of plague.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 GTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVLGTAIQGQIV
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STRAIN-LTZ / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed-11677609;
MCCLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 477;
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18.7%; Pred. No. 0.022;
tive 78; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                         Nature 413.523-527(2001).
EMBL; AJ414145; CAC89838.1; -.
InterPro; IPR001927; Na/Gal_symp.
TIGREAMS; TIGR00792; gph; 1.
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Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      477 AA;
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Matches 73; Conserv
                                                                  SEQUENCE FROM N.A.
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01-MAR-2002 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 TEQTERDSATAYRMTVEVLGTVLGTAIQGQI---VGQADTPCFQDFNSSTVASQSANHTH 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
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                                                            "Complete genome sequence of Salmonella enterica serovar Typhimurium
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BEDLINE-21074935; PubMed-11205551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Bosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                            59;
                                                                                                                                                                                                                                              ; Score 131.5; DB 16; Length 444; Pred. No. 0.025; 60; Mismatches 160; Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRRQNKKAL 434
                                                                                                                                                                                    Hypothetical protein, Complete proteome.
SEQUENCE 444 AA; 49680 MW; A0E6BFD55C60700E CRC64;
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Last annotation update)
shikimate.
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                                                                                                              EMBL; AE008890; AAL22905.1; .
InterPro; IPR001927; Na/Gal_symp.
Hynorhatical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Putative transport protein, SHIA OR 23138 OR ECS2778.
                     Ryan E., Sun H., Florea L., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 19.8<sup>1</sup>
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                      Nature 413:852-856(2001)
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NCBI_TaxID=83334;
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